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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/024,066	12/18/2001	Loren J. Field	7037-450	3713
7590	07/20/2005			
Kenneth A. Gandy Woodard, Emhardt, Naughton, Moriarty & McNett Bank One Center/Tower, Suite 3700 111 Monument Circle Indianapolis, IN 46204-5137				EXAMINER SULLIVAN, DANIEL M
				ART UNIT 1636
				PAPER NUMBER DATE MAILED: 07/20/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

<b>Office Action Summary</b>	<b>Application No.</b>	<b>Applicant(s)</b>	
	10/024,066	FIELD ET AL.	
	<b>Examiner</b>	<b>Art Unit</b>	
	Daniel M. Sullivan	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

#### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

1) Responsive to communication(s) filed on 06 July 2005.  
 2a) This action is **FINAL**.                            2b) This action is non-final.  
 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

4) Claim(s) 51 and 52 is/are pending in the application.  
 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.  
 5) Claim(s) \_\_\_\_\_ is/are allowed.  
 6) Claim(s) 51 and 52 is/are rejected.  
 7) Claim(s) \_\_\_\_\_ is/are objected to.  
 8) Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

9) The specification is objected to by the Examiner.  
 10) The drawing(s) filed on \_\_\_\_\_ is/are: a) accepted or b) objected to by the Examiner.  
     Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
     Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).  
 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
 a) All    b) Some \* c) None of:  
 1. Certified copies of the priority documents have been received.  
 2. Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.  
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

1) Notice of References Cited (PTO-892)  
 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)  
 3) Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)  
     Paper No(s)/Mail Date \_\_\_\_\_

4) Interview Summary (PTO-413)  
     Paper No(s)/Mail Date. 7/12/05.  
 5) Notice of Informal Patent Application (PTO-152)  
 6) Other: sequence alignments.

### **DETAILED ACTION**

This Non-Final Office Action is a response to the Paper filed 6 July 2005 in response to the Final Office Action mailed 8 February 2005. Claims 43-59 and 63-84 had been withdrawn from consideration and claims 20-28, 49, 50 and 51-62 were considered in the 8 February Office Action. Claims 20-28, 49, 50, 53-62 and 63-84 were canceled and claims 51 and 52 were amended in the 6 July Paper. Claims 51 and 52 are pending.

Finality of the previous Office Action is hereby **withdrawn** in view of the new grounds for rejection set forth herein below.

#### ***Response to Amendment***

Rejection of claims 20-28, 49, 50 and 53-62 is rendered moot by the cancellation thereof.

Objection to claims 51 and 52 is withdrawn in view of the amendments thereto.

#### ***Claim Rejections - 35 USC § 103***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

Art Unit: 1636

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claim 51 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.* (1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J. Physiol.* 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession No. M86182 (hereinafter, M86182).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 2.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645 and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic acid comprising the amino acid sequence of SEQ ID NO: 2. However, Soonpaa *et al.* teaches, “[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has

been invested to develop strategies to induce cardiomyocyte proliferation" (first full paragraph in the left column on page 2644) and "[t]his study represents an initial pragmatic effort to test candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis" (third paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth (see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption thereto). Li *et al.* concludes, "[f]uture experiments designed to induce forced expression of these [including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to strategies for improving the prognosis of this disease" (paragraph bridging pages H821-H822).

M86182 teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 2 (see the attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the cyclin D2 nucleic acid disclosed in M86182 the cardiomyocytes of which would be the same as the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte proliferation and that the transgenic animal disclosed therein provides a means to test candidate genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in hypertrophy should offer an approach to determine the role of these genes and may lead to

therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse comprising a nucleic acid encoding the instant SEQ ID NO: 2 as disclosed in M86182.

Absent evidence to the contrary, one would have a reasonable expectation of success in combining these teachings in view of the well-established nature of transgenic animal technology and the guidance for making a transgenic animal expressing a cyclin D protein provided in Soonpaa *et al.*

For these reasons, the invention of claim 51, as a whole, would have been obvious to one of ordinary skill in the art at the time the invention was made.

Claim 52 is rejected under 35 U.S.C. 103(a) as being unpatentable over Soonpaa *et al.* (1997) *J. Clin. Invest.* 99:2644 (previously made of record) in view of Li *et al.* (1998) *Am. J. Physiol.* 275:H814-H822 and further in view of ENTREZ Nucleotide Database Entry Accession No. X68452 (hereinafter, X68452).

The claim is directed to a cardiomyocyte cell including an introduced nucleic acid molecule wherein the molecule encodes the polypeptide set forth as SEQ ID NO: 4.

Soonpaa *et al.* teaches overexpression of a cyclin D protein in cardiomyocytes of a transgenic mouse (see especially the paragraph bridging the left and right columns on page 2645 and the paragraph bridging the left and right columns on page 2647).

Soonpaa does not teach overexpression of an introduced nucleic acid encoding a nucleic acid comprising the amino acid sequence of SEQ ID NO: 4. However, Soonpaa *et al.* teaches, “[g]iven the therapeutic potential of regenerative myocardial growth, considerable effort has been invested to develop strategies to induce cardiomyocyte proliferation” (first full paragraph in

the left column on page 2644) and “[t]his study represents an initial pragmatic effort to test candidate genes which may participate in the regulation of cardiomyocyte DNA synthesis” (third paragraph on page 2645).

Li *et al.* teaches that cyclin D2 is upregulated during cardiomyocyte hypertrophic growth (see especially the Abstract, the paragraph bridging pages H816-H817, Figure 2 and the caption thereto). Li *et al.* concludes, “[f]uture experiments designed to induce forced expression of these [including cyclin D2] molecules in cardiomyocytes should offer an approach to determine the precise role of cell cycle regulatory molecules in cardiomyocyte hypertrophy and may lead to strategies for improving the prognosis of this disease” (paragraph bridging pages H821-H822).

X68452 teaches a cyclin D2 nucleic acid encoding the instant SEQ ID NO: 4 (see the attached sequence alignment).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to produce a transgenic mouse according to the teachings of Soonpaa *et al.* using the cyclin D2 nucleic acid disclosed in X68452, the cardiomyocytes of which would be the same as the cardiomyocytes of the instant claims. Motivation to combine these teachings comes from Soonpaa *et al.*, who teaches the desirability of identifying regulators of cardiomyocyte proliferation and that the transgenic animal disclosed therein provides a means to test candidate genes that may participate in regulation of cardiomyocyte DNA synthesis. Further motivation comes from the teachings of Li *et al.*, which establish the upregulation of cyclin D2 during cardiomyocyte hypertrophic growth and teach that forced overexpression of genes upregulated in hypertrophy should offer an approach to determine the role of these genes and may lead to

therapeutic strategies. Thus, the skilled artisan would clearly be motivated to make a mouse comprising a nucleic acid encoding the instant SEQ ID NO: 4 as disclosed in X68452.

Absent evidence to the contrary, one would have a reasonable expectation of success in combining these teachings in view of the well-established nature of transgenic animal technology and the guidance for making a transgenic animal expressing a cyclin D protein provided in Soonpaa *et al.*

For these reasons, the invention of claim 52, as a whole, would have been obvious to one of ordinary skill in the art at the time the invention was made.

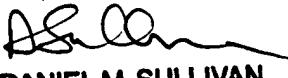
### ***Conclusion***

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel, Ph.D. can be reached on 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Daniel M. Sullivan, Ph.D.  
Examiner  
Art Unit 1636



DANIEL M. SULLIVAN  
PATENT EXAMINER





Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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DEFINITION	Mouse cyclin 2 (CYL 2)	VERSION	1
ACCESSION	M86182	NEW WORDS	GI:192879
VERSION	M86182.1	DEFINITION	Mouse cyclin 2 (house mouse)
RESULT 3			
MUSCYL2A	MUSCYL2A	LOCUS	US-10-024-066-2 (1-289) x MUSCYL2A (1-1034)
DEFINITION	Mouse cyclin 2 (CYL 2)	VERSION	1
ACCESSION	M86182	NEW WORDS	GI:192879
VERSION	M86182.1	DEFINITION	Mouse cyclin 2 (house mouse)

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Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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Pred. No. is the number of results predicted by chance to have a

## SUMMARIES

## ALIGNMENTS

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CM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 20:22:56 ; Search time 189 Seconds (without alignments)

Scoring table: BLASTNG2

Title: US-10-024-066-2

Perfect score: 1513

Sequence: 1 MEIJCEVDPVRRAVDPRLN.....KSVEDPDQATTPPDVRYDVL 289

Scoring table: BLASTNG2

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Dgapext 6.0 , Dgapext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database :

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1: /cgn2_6/ptodata/1/ina/5A..COMB..seq:*
2: /cgn2_6/ptodata/1/ina/5B..COMB..seq:*
3: /cgn2_6/ptodata/1/ina/6A..COMB..seq:*
4: /cgn2_6/ptodata/1/ina/6B..COMB..seq:*
5: /cgn2_6/ptodata/1/ina/PCFTUS..seq:*
6: /cgn2_6/ptodata/1/ina/backfFile1.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1380	91.2	1129	4	US-09-920-760-3		Sequence 3, Appli
2	1380	91.2	1911	2	US-08-246-361A-3		Sequence 3, Appli
3	1380	91.2	6478	4	US-09-919-497-4		Sequence 4, Appli
4	1380	91.2	6478	4	US-09-919-016-256		Sequence 256, App
5	1380	91.2	6479	4	US-09-919-016-2149		Sequence 2149, Ap
6	13357	89.7	1970	2	US-08-464-517-3		Sequence 3, Appli
7	13357	89.7	1970	3	US-08-453-772-3		Sequence 3, Appli
8	13357	89.7	1970	5	PC-US91000000-3		Sequence 3, Appli
9	91.5	89.7	1970	5	PC-US91000000-3		Sequence 3, Appli
10	975.5	64.5	1462	2	US-08-464-517-30		Sequence 30, Appli
11	975.5	64.5	1462	2	US-08-246-361A-30		Sequence 30, Appli
12	975.5	64.5	1462	3	US-08-463-772-30		Sequence 30, Appli

## ALIGNMENTS

RESULT 1  
US-09-920-760-3  
; Sequence 3, Application US/09920760  
; Patent No. 6492173  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowpert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION  
; FILE REFERENCE: RTS-0275  
; CURRENT APPLICATION NUMBER: US/09-920-760-0  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 3  
; LENGTH: 1129  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (156) ... (1025)  
US-09-920-760-3

Alignment Scores:  
Pred. No. : 3\_156-180  
Score: 1380.00  
Percent Similarity: 97.24%  
Best Local Similarity: 91.21%  
Query Match: 91.21%  
DB: 4  
Gaps: 2  
Length: 1129  
Matches: 266  
Mismatches: 6  
Indels: 2  
US-10-024-066-2 (1-289) x US-09-920-760-3 (1-1129)  
QY 1 MetGluLeuLeuCysCysGluValAspProAspArgArgAlaValProAspArgAspLeu 20  
Db 156 ATGGCTGCTGCGACGGTGCACGGCTGCGACGGGACGGAACTG 215  
QY 21 Leu--GluAspPArgValLeuGluAsnLeuThrIleGluGluArgTyrLeuProGln 39

6 GenCore version 5.1.6  
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7 Q3OM protein - nucleic search, using frame Plus P2n model  
 Run on: July 13, 2005, 17:34:44 ; Search time 596.5 Seconds  
 (without alignments)  
 2868.072 Million cell updates/sec

8 Title: US-10-024-066-2  
 Perfect score: 1 MELLCCEDVPVRRAVFDRLN.....KSVPDPDQATTPTDVRDVDL 289  
 Sequence: BLOSUM62

9 Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapext 7.0  
 Delop 6.0 , Delext 7.0

10 Searched: 4390206 seqs, 2959870667 residues  
 Total number of hits satisfying chosen parameters: 8780412

11 Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

12 Command line parameters:  
 MODB1=frame+p2n.model -DB=x11  
 O=1/cgn2.1/ISPTO.spoof.h/US10024066/runat.13072005.140959.28036/app\_query.Fasta\_1.910  
 DB=N/geneseq -QFMT=fatap -SUFFIX=rng -MINMATCH=0.1 -LOOFCT=0  
 DOCA1IGN=200 -THR SCORE=pct -THR MAX=1 -MTRX=biolum62 -START=-1 -END=-1 -MTRX=human40.cdi -LIST=45  
 OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
 USER=US10024066 @CGN 1.1 586 @runat.13072005.140959.28036 -NCPU=6 -ICPU=3  
 NO\_MMVA -LARGEQUERY -NEG SCORES=0 -WATT DSFBLOCK=100 -LONGLOG  
 DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

13 Ada02736 Mouse Ccn  
 Adb72474 Mouse Ccn  
 Adc5216 Mouse Ccn  
 Adm74331 Murine C  
 Ada0740 Human Ccn  
 Adb72478 Human Ccn  
 Adc5220 Human Ccn  
 Adm74335 Human ccy  
 Aad02407 Human cyc  
 Ac650565 DNA encod  
 Add18442 Human pro  
 Aaq1874 Cyclin D1  
 Adi31696 Human cde  
 Abi52484 Human end  
 Abi66613 Lung canc  
 Abv94470 Breast ca  
 Abn05109 Gene #160  
 Ada0739 Human CNN  
 Adb72477 Human Ccn  
 Adc5219 Human cy  
 Adi18145 Leukemia  
 Adi182848 Human PR  
 Adh28853 Human chg  
 Adm74334 Human Ccn  
 Ado19119 Human PR  
 Ace34507 Gene enco  
 Adf16507 Novel huc  
 Adh17148 Human cyc  
 Adi182848 Human PR  
 Adp07302 Human Ccn  
 Ado19119 Human PR  
 Ado19117 Human PR  
 Adp4150 Human PR  
 Adp3073 PRO POLY  
 Abx61004 Human Cdn  
 Adj56260 Human Cdn  
 Aaq53198 Human cyc  
 Adf14433 Leukemia  
 Adf14444 Leukemia  
 Aah57370 Human hea

## ALIGNMENTS

**RESULT 1**  
 ADA02737  
 ID ADA02737 standard; cDNA; 870 BP.  
 XX  
 AC ADA02737;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Mouse *Ccnd2* carcinoma associated coding sequence, SEQ ID NO:1255.  
 XX  
 KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast  
 KW prostate; lymphoma; leukaemia; cyclostatis; gene therapy; drug screening;  
 KW gene; ss.  
 XX

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	ID			
1	1513	100.0	870	9	ADA02737		Ada02737 Mouse Ccm
2	1513	100.0	870	10	ADBB2475		Adb2475 Mouse Ccm
3	1513	100.0	870	10	ADCC5217		Adc5217 Mouse Ccm
4	1513	100.0	870	12	ADM4332		Adm4332 Murine ccm
5	1513	100.0	875	5	ADNO2406		Adn02406 Mouse ccm

MEETINGS



GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 23:40:22 ; Search time 669.5 Seconds

(without alignments)

2710.137 Million cell updates/sec

Title: US-10-024-066-4

Perfect score: 1501

Sequence: 1 MELLCHEVDPVERAVDRNL.....KSEDELDQASTPTDVRDIDL 289

Scoring table: BLOSSUM62

Xgapext 10.0 , Xgapext 0.5

Ygapext 10.0 , Ygapext 0.5

Fgapext 6.0 , Fgapext 7.0

Delpop 6.0 , Delext 7.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-MDBL:frame_p2n.model -DEV=x1h
-O: cgm2_1/USP0 spool h/US10024066/runat_13072005_141002_28138/app_query.fasta_1_910
-DB_PUBLISHED_Applications_NA -OPMT=fabrap SUPPIX=rtDB -WINMATCH=0.1
-LOOPBXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=61.0sum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TMR MIN=0 -ALIGN=15 -MDBR=LOCAL OUTENT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=1000000000 -NCPU=3 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

## Database :

Published\_Applications\_NA:\*

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1: /cgm2_6/podata/1/pubpna/us07_PUBCOMB.seq:*
2: /cgm2_6/podata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgm2_6/podata/1/pubpna/us05_NEW_PUB.seq:*
4: /cgm2_6/podata/1/pubpna/us06_PUBCOMB.seq:*
5: /cgm2_6/podata/1/pubpna/us07_NEW_PUB.seq:*
6: /cgm2_6/podata/1/pubpna/PCRS5_PUBCOMB.seq:*
7: /cgm2_6/podata/1/pubpna/us08_PUBCOMB.seq:*
8: /cgm2_6/podata/1/pubpna/us09_PUBCOMB.seq:*
9: /cgm2_6/podata/1/pubpna/us09B_PUBCOMB.seq:*
10: /cgm2_6/podata/1/pubpna/us09C_PUBCOMB.seq:*
11: /cgm2_6/podata/1/pubpna/us09_NNEW_PUB.seq:*
12: /cgm2_6/podata/1/pubpna/us09_NNEW_PUB.seq:*
13: /cgm2_6/podata/1/pubpna/us10_PUBCOMB.seq:*
14: /cgm2_6/podata/1/pubpna/us10_PUBCOMB.seq:*
15: /cgm2_6/podata/1/pubpna/us10C_PUBCOMB.seq:*
16: /cgm2_6/podata/1/pubpna/us10D_PUBCOMB.seq:*
17: /cgm2_6/podata/1/pubpna/us10E_PUBCOMB.seq:*
18: /cgm2_6/podata/1/pubpna/us10F_PUBCOMB.seq:*
19: /cgm2_6/podata/1/pubpna/us10G_PUBCOMB.seq:*
20: /cgm2_6/podata/1/pubpna/us10H_PUBCOMB.seq:*
21: /cgm2_6/podata/1/pubpna/us10I_PUBCOMB.seq:*
22: /cgm2_6/podata/1/pubpna/us10_NNEW_PUB.seq:*
23: /cgm2_6/podata/1/pubpna/us11_PUBCOMB.seq:*
24: /cgm2_6/podata/1/pubpna/us11_NNEW_PUB.seq:*
25: /cgm2_6/podata/1/pubpna/us10_NNEW_PUB.seq:*
26: /cgm2_6/podata/1/pubpna/us10_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1501	100.0	870	11	US-09-997-722-6	Sequence 6, Appli
2	1501	100.0	873	13	US-10-024-066-3	Sequence 3, Appli
3	1501	100.0	1898	16	US-10-210-120-14	Sequence 14, Appli
4	1501	100.0	1898	22	US-10-909-035-14	Sequence 14, Appli
5	1501	100.0	1911	18	US-10-641-643-1022	Sequence 1022, Appli
6	1501	100.0	6478	9	US-09-919-497-4	Sequence 4, Appli
7	1501	100.0	6478	9	US-09-954-456-1923	Sequence 1923, Appli
8	1501	100.0	6478	9	US-09-880-107-1607	Sequence 1607, Appli
9	1501	100.0	6478	11	US-09-997-722-5	Sequence 5, Appli
10	1501	100.0	6478	15	US-10-177-581-121	Sequence 121, Appli
11	1501	100.0	6478	21	US-10-843-641A-461	Sequence 4950, Appli
12	1501	100.0	6478	17	US-10-440-464-147	Sequence 147, Appli
13	1501	100.0	6480	17	US-10-370-715B-181	Sequence 181, Appli
14	1501	100.0	6480	20	US-10-378-715B-181	Sequence 62, Appli
15	1501	100.0	6508	13	US-10-044-090-4	Sequence 4, Appli
16	1501	100.0	6508	15	US-10-084-817-66	Sequence 66, Appli
17	1501	100.0	870	11	US-09-997-722-3	Sequence 3, Appli
18	1380	91.9	870	13	US-10-024-066-1	Sequence 1, Appli
19	1380	91.9	876	13	US-10-024-066-1	Sequence 2, Appli
20	1380	91.9	1255	11	US-09-997-722-12	Sequence 12, Appli
21	998	66.5	1053	9	US-09-778-927A-12	Sequence 1365, Appli
22	925	61.6	4242	18	US-10-641-643-1365	Sequence 566, Appli
23	925	61.6	4244	9	US-09-964-824A-566	Sequence 1594, Appli
24	925	61.6	4244	9	US-09-954-456-1594	Sequence 213, Appli
25	925	61.6	4244	9	US-09-967-768A-213	Sequence 5869, Appli
26	925	61.6	4244	21	US-10-843-641A-4621	Sequence 6358, Appli
27	925	61.6	4244	21	US-10-843-641A-5869	Sequence 6358, Appli
28	925	61.6	4244	21	US-10-843-641A-6358	Sequence 6358, Appli
29	925	61.6	4306	17	US-10-295-027-635	Sequence 67, Appli
30	925	61.6	4306	18	US-10-302-812-67	Sequence 423, Appli
31	925	61.6	4397	17	US-10-641-049-423	Sequence 27, Appli
32	913	60.8	888	16	US-10-004-113-27	Sequence 30, Appli
33	913	60.8	888	16	US-10-004-113-30	Sequence 15, Appli
34	913	60.8	888	17	US-10-394-948-15	Sequence 18, Appli
35	913	60.8	888	17	US-10-394-948-18	Sequence 10, Appli
36	913	60.8	1256	21	US-10-630-880-10	Sequence 10, Appli
37	913	60.8	1325	15	US-10-007-926-10	Sequence 10, Appli
38	913	60.8	1325	16	US-10-510-279	Sequence 29, Appli
39	913	60.8	1325	16	US-10-004-113-29	Sequence 5, Appli
40	913	60.8	1325	17	US-10-133-937-5	GENERAL INFORMATION:
41	913	60.8	1325	17	US-10-172-118-661	APPLICANT: Morris, David
42	913	60.8	1325	17	US-10-159-563-5	TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
43	913	60.8	1325	17	US-10-394-948-17	FILE REFERENCE: A-71171/RMS/DCP
44	913	60.8	1325	18	US-10-332-887-661	CURRENT FILING DATE: 2001-11-30
45	913	60.8	1454	18	US-10-152-3152A-2187	PRIOR APPLICATION NUMBER: US 09/747,377

## ALIGNMENTS

RESULT 1  
 US-09-772-6  
 Sequence 6, Application US/09997722  
 Publication No. US20040072154A1  
 CURRENT FILING DATE: 2001-11-30  
 PRIORITY FILING DATE: 2000-12-22  
 PRIORITY APPLICATION NUMBER: US 09/747,377  
 NUMBER OF SEQ ID NOS: 301  
 NUMBER OF SEQ ID NOS: 301

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus p2n model

Run on: July 13, 2005, 20:22:56 ; Search time 1.89 Seconds  
 (without alignments)  
 2502.032 Million cell updates/sec

Title: US-10-024-066-4  
 Perfect score: 1501  
 Sequence: 1 MBLCHEVDPVRAVRDRNL.....KSEDDELDOASTPTDVRDIDL 289

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delet	7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:  
 -MDBL=frame+\_P2n.model -DEV=xlh  
 -O= cgm2 1/USP0 spool h/US1024066/runat 13072005 141001 28069/app query.fasta 1.910

-FGA~~PE~~XT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*

2: /cgm2\_6/pctodata1/1/ina/5B COMB.seq:\*

3: /cgm2\_6/pctodata1/1/ina/6A COMB.seq:\*

4: /cgm2\_6/pctodata1/1/ina/6B COMB.seq:\*

5: /cgm2\_6/pctodata1/1/ina/PCTUS COMB.seq:\*

6: /cgm2\_6/pctodata1/1/ina/backfile1.seq:\*

Result No.	Score	Query		Length	DB	ID	Description
		Match	Length				
1	1501	100.0	1129	4	US-09-920-760-3		Sequence 3, Appli
2	1501	100.0	1911	2	US-09-246-361A-3		Sequence 3, Appli
3	1501	100.0	1911	4	US-09-023-655-1022		Sequence 1022, Ap
4	1501	100.0	6478	4	US-09-919-497-4		Sequence 4, Appli
5	1501	100.0	6478	4	US-09-016-549-256		Sequence 256, Ap
6	1501	100.0	6479	4	US-09-949-016-2149		Sequence 2149, Ap
7	1471	98.0	1970	2	US-08-464-517-3		Sequence 3, Appli
8	1471	98.0	1970	3	US-08-463-772-3		Sequence 3, Appli
9	1471	98.0	1970	5	PCT-US93-05000-3		Sequence 3, Appli
10	1051.5	70.1	1462	2	US-08-464-517-30		Sequence 30, Appli
11	1051.5	70.1	1462	2	US-08-246-161A-30		Sequence 30, Appli
12	1051.5	70.1	1452	2	US-08-463-272-30		Sequence 30, Appli

13	1024.5	68.3	1462	5	PCT-US93-05000-30.
14	927	61.8	4453	1	US-08-770-761A-4
15	927	61.8	4453	1	US-08-770-761A-5
15	927	61.8	4621	1	US-08-770-761A-1
16	927	61.8	4621	1	US-08-770-761A-1
17	925	61.6	4221	1	US-07-947-120-7
18	925	61.6	4221	1	US-08-472-893A-7
19	925	61.6	4221	3	US-08-947-492-7
20	925	61.6	4242	4	US-09-023-655-1-365
21	925	61.6	4244	3	US-08-460-694-1
22	925	61.6	4244	3	US-08-460-744-1
23	925	61.6	4244	3	US-07-667-711B-1
24	913	60.8	1325	1	US-08-306-692B-51
25	911.5	60.7	1962	2	US-08-246-361A-5
26	911.5	60.7	1962	4	US-09-023-655-1-023
27	911.5	60.7	1962	4	US-09-814-912A-59
28	865	57.6	1325	2	US-08-464-517-1
29	865	57.6	1325	2	US-08-246-361A-1
30	865	57.6	1325	3	US-08-463-772-1
31	865	57.6	1325	5	PCT-US93-05000-1
32	801.5	53.4	1926	2	US-08-464-517-5
33	801.5	53.4	1926	3	US-08-463-772-5
34	801.5	53.4	1926	5	PCT-US93-05000-5
35	522	34.8	2022	2	US-08-464-517-2
36	522	34.8	2022	2	US-08-246-361A-32
37	522	34.8	2022	3	US-08-463-772-32
38	426	28.4	1901	5	PCT-US93-05000-32
39	377.5	25.1	36302	4	US-09-949-016-11998
40	377.5	25.1	36302	4	US-09-949-603-1-3891
41	314.5	21.0	863	3	US-08-728-603-18
42	314.5	21.0	32207	2	US-08-770-379-20
43	314.5	21.0	32207	3	US-08-557-662A-20
44	314.5	21.0	32207	3	US-09-330-371A-20
45	280.5	18.7	601	4	US-09-949-016-23242

## ALIGNMENTS

RESULT 1  
US-09-920-760-3  
Sequence 3, Application US/09920  
; Patent No. 692173  
; GENERAL INFORMATION:  
APPLICANT: Alex M. Cowert  
TITLE OF INVENTION: ANTISENSE MC  
FILED REFERENCE: RIS-075  
CURRENT APPLICATION NUMBER: US/0  
CURRENT FILING DATE: 2001-08-01  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 3  
LENGTH: 1129  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
;  
US-09-920-760-3  
US-09-920-760-3

Alignment Scores:					
Pred. No.:	2.72e-193	Length:	1129		
Score:	1501.00	Matches:	289		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	4	Gaps:	0		
US-10-024-066-4 (1-289) x US-09-920-760-3 (1-1129)					
Qy	1 MetGluLeuLeuGluValAspProValArgArgAlaVal				
Db	156 ATGGAGCTCTGTGCAACAGGGTGACCCGTCAGGGCCGTC				
Qy	21 LeuArgAspAspArgValLeuGlnAsnLeuLeuThrIleGluGlu				

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 17:34:44 ; Search time 596.5 Seconds  
(without alignment(s))

2868.07 Million cell updates/sec

Perfect score: 1501

Sequence: 1 MELLCHEVDPVRAVDRNLT.....KSEDELDQASTPTDVRDIDL 289

Scoring table: BLOSUM62

Xgapext 0.5  
Ygapext 0.5  
Ygapext 0.5  
Fgapext 7.0  
Dgapext 7.0  
Delext 7.0

Searched: 4390206 Seqs, 2939870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL:frame\_p2n.model -DEV=x1h  
-O /cgn2.1 /USPPTO spool/h/US01024066/runat\_13072005\_140959\_28016/app/query.fasta\_1.910  
-DB=N Geneseq -OFNT=fastap -SUPPFX=rng -MIMMATCH=0.1 -LOOPEXT=0  
-DNTS=bits -START=1 -END=1 -MATRIX=b10sum62 -TRANS=human40.cgi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNC=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US01024066 @CGN\_1-516 @runat\_13072005\_140959\_28016 -NCPU=6 -ICP0=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6  
-PGAPEXT=7 -YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1900s:\*

2: Geneseqn1900s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001ab:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002ab:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003ab:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004ab:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1501	100.0	870	9 ADA02740	Ada02740 Human CCN
2	1501	100.0	870	10 AD572478	Ad572478 Human CCN
3	1501	100.0	870	10 ADC85220	Adc85220 Human Ccn
4	1501	100.0	870	12 ADM74335	Adm74335 Human car
5	1501	100.0	873	5 ADD02407	Ad02407 Human cyc

## ALIGNMENTS

6	1501	100.0	1129	10 ACA60565	ACA60565 DNA encod
7	1501	100.0	1898	10 ADD18442	Add18442 Human pro
8	1501	100.0	1911	2 AQQ1874	Aqq1874 Cyclin D2
9	1501	100.0	1911	11 AD31696	Ad31696 Human cdn
10	1501	100.0	6478	6 ABK5484	Abk5484 Human end
11	1501	100.0	6478	6 ABLG6613	Abi66613 Lung canc
12	1501	100.0	6478	6 ABV94470	Abv94470 Breast ca
13	1501	100.0	6478	6 ABN9109	Abn9109 Gene #160
14	1501	100.0	6478	9 ADA2739	Ada2739 Human CCN
15	1501	100.0	6478	10 AD572477	Ad572477 Human CCN
16	1501	100.0	6478	10 AD85219	Ad85219 Human Ccn
17	1501	100.0	6478	10 AD181445	Ad181445 Leukaemia
18	1501	100.0	6478	10 AD28853	Ad28853 Human chr
19	1501	100.0	6478	12 ADM74334	Adm74334 Human car
20	1501	100.0	6478	12 AD019119	Ad019119 Human PRO
21	1501	100.0	6480	8 ACF4507	ACF4507 Gene enco
22	1501	100.0	6480	10 AD776507	Ad776507 Novel hum
23	1501	100.0	6480	12 ADH17148	Adh17148 Human cyc
24	1501	100.0	6480	12 ADH82848	Adh82848 Human PRO
25	1501	100.0	6480	12 ADP07302	Adp07302 Human CCN
26	1501	100.0	6480	12 ADZ020473	Adz020473 Human PRO
27	1501	100.0	6480	12 ADG19115	Adg19115 Human PRO
28	1501	100.0	6480	12 ADG19117	Adg19117 Human PRO
29	1501	100.0	6480	13 ADG54150	Adg54150 Human PRO
30	1501	100.0	6480	13 ADP23073	Adp23073 PRO polyP
31	1501	100.0	6508	8 ABX63004	Abx63004 Human cdn
32	1501	100.0	6508	10 AD56260	Ad56260 Human cdn
33	1495	99.6	6598	10 AD81443	Ad81443 Leukaemia
34	1495	99.6	6598	10 AD81444	Ad81444 Leukaemia
35	1491	99.3	1911	2 AAQ3198	Aaq3198 Human cyc
36	1436	95.7	6518	4 AAH7370	Aah7370 Human hea
37	1380	91.9	870	9 ADA02737	Ad02737 Human Ccn
38	1380	91.9	870	10 ADB72475	Adb72475 Mouse Ccn
39	1380	91.9	870	10 ADP85217	Adp85217 Mouse Ccn
40	1380	91.9	870	12 ADM74332	Adm74332 Murine ca
41	1380	91.9	876	5 ADD2406	Ad2406 Murine cyc
42	1380	91.9	1285	9 ADAB2736	Adb2736 Murine Ccn
43	1380	91.9	1255	10 ADP72474	Adp72474 Murine Ccn
44	1380	91.9	1255	10 ADG85216	Adg85216 Murine Ccn
45	1380	91.9	1255	12 ADM74331	Adm74331 Murine ca

## RESULTS

1	ADA02740	Standard; cdna;	870 BP.
2	XX		
3	AC		
4	XX		
5	DT	06-NOV-2003 (first entry)	
6	DB	Human CCND2 carcinoma associated coding sequence, SEQ ID NO:1258.	
7	XX		
8	XX		
9	XX		
10	XX		
11	XX		
12	XX		
13	XX		
14	OS	Homo sapiens.	
15	XX		
16	PR	26-DEC-2002; 2002WO-US041414.	
17	XX	26-DEC-2001; 2001US-00035832.	
18	XX	(SAGR-) SAGRES DISCOVERY.	
19	PA	26-DEC-2002; 2002WO-US041414.	
20	PR	26-DEC-2001; 2001US-00035832.	
21	XX	W02003057146-A2.	
22	XX	17-JUL-2003.	

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CM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 19:05:08 ; search time 4889.5 Seconds  
(without alignments)  
2864.0006 Million cell updates/sec

Title: US-10-024-066-4

Perfect score: 1501

Sequence: 1 MELCHEVDPVRRAVDRNL.....KSDELDOQASPTDVRIDL 289

Scoring table: BLASTN62

xgapop 10.0 xgapext 0.5  
Ygapop 10.0 / Ygapext 0.5  
Pgapop 6.0 / Pgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-rMODEL=frame\_p2n.model -DEV=rxlib  
-Q= /cgn2\_1 /USP0\_spool1\_h /US10024066/runat\_13072005\_140959\_28043/app\_query.fasta\_1.910  
-DB=GenEmbl -DEFINITION= -PREFIX= -MINMATCH=0.1 -LOOPCJ=0 -LOOPCT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCOR=pct -THR MAX=100 -THR MIN=0 -ALIGN=N -MODE=LOCAL  
-OUTFMT=0to -NORM=ext -HEAPSIZ=0 -MAXLEN=2000000000  
-USRP=US-0241066 @CGN\_1.1 -HEAPSIZ=0 @runat\_13072005\_140959\_28043 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NSG -SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN -TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:  
1: gb\_ha:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_on:  
5: gb\_ov:  
6: gb\_dat:  
7: gb\_bh:  
8: gb\_pl:  
9: gb\_dr:  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 13, 2005, 19:05:08 ; Search time 4889.5 Seconds

(without alignments)

2864.006 Million cell updates/sec

Title: US-10-024-066-2

Perfect score: 1513

Sequence: MELLCEEVDPYRRAVPDRNL.....ESVVEDPQATTPTDYRDVDSL 289

Scoring table: BLOSUM62

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1513	100.0	1255	10	MUSDCYC	Mouse D-typ

#### ALIGNMENTS

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6	1482.5	98.0	1415	10	RATCYCLD2A		
7	1469.5	97.1	1120	10	RATCYCLND2		
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12	1380	91.2	1911	6	AR093074	Homo sapi	
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20	1380	91.2	6478	6	AX779844	Sequence	
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SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Morris,D.W. and Englehardt,E.K.				
JOURNAL	Novel compositions and methods for cancer				
	Patent: WO 03008583-A 1255 30-JAN-2003;				
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RESULTS 1	AX695628	870 bp	DNA	linear	PAT 31-MAR-2003
LOCUS	AX695628	Sequence	1255	from Patent	WO03008583.
DEFINITION	AX695628	Sequence	1255	from Patent	WO03008583.
ACCESSION	AX695628	Sequence	1255	from Patent	WO03008583.
VERSION	AX695628.1	Sequence	1255	from Patent	WO03008583.
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Morris,D.W. and Englehardt,E.K.				
JOURNAL	Novel compositions and methods for cancer				
	Patent: WO 03008583-A 1255 30-JAN-2003;				
FEATURES	Sagres Discovery (US)				
source	Location/Qualifiers				
	1. .870				
ORIGIN	/organism="Mus musculus"				
	/mol type="unassigned DNA"				
	/db_xref="taxon:10090"				

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